

Christian Rinke

List of Publications by Year in descending order

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Version: 2024-02-01

45
papers

14,125
citations

117453

34
h-index

182168

51
g-index

61
all docs

61
docs citations

61
times ranked

12431
citing authors

#	ARTICLE	IF	CITATIONS
1	A standardized bacterial taxonomy based on genome phylogeny substantially revises the tree of life. Nature Biotechnology, 2018, 36, 996-1004.	9.4	2,615
2	Insights into the phylogeny and coding potential of microbial dark matter. Nature, 2013, 499, 431-437.	13.7	2,239
3	Minimum information about a single amplified genome (MISAG) and a metagenome-assembled genome (MIMAG) of bacteria and archaea. Nature Biotechnology, 2017, 35, 725-731.	9.4	1,512
4	Recovery of nearly 8,000 metagenome-assembled genomes substantially expands the tree of life. Nature Microbiology, 2017, 2, 1533-1542.	5.9	1,465
5	A complete domain-to-species taxonomy for Bacteria and Archaea. Nature Biotechnology, 2020, 38, 1079-1086.	9.4	883
6	GTDB: an ongoing census of bacterial and archaeal diversity through a phylogenetically consistent, rank normalized and complete genome-based taxonomy. Nucleic Acids Research, 2022, 50, D785-D794.	6.5	662
7	An environmental bacterial taxon with a large and distinct metabolic repertoire. Nature, 2014, 506, 58-62.	13.7	530
8	A genomic catalog of Earth's microbiomes. Nature Biotechnology, 2021, 39, 499-509.	9.4	457
9	Comparative Genomic Analysis of the Class Epsilonproteobacteria and Proposed Reclassification to Epsilonbacteraeota (phyl. nov.). Frontiers in Microbiology, 2017, 8, 682.	1.5	409
10	Microbial dark matter ecogenomics reveals complex synergistic networks in a methanogenic bioreactor. ISME Journal, 2015, 9, 1710-1722.	4.4	360
11	Obtaining genomes from uncultivated environmental microorganisms using FACS-based single-cell genomics. Nature Protocols, 2014, 9, 1038-1048.	5.5	243
12	A standardized archaeal taxonomy for the Genome Taxonomy Database. Nature Microbiology, 2021, 6, 946-959.	5.9	198
13	Phylogeny and physiology of candidate phylum "Atribacteria" (OP9/JJ1) inferred from cultivation-independent genomics. ISME Journal, 2016, 10, 273-286.	4.4	166
14	Decontamination of MDA Reagents for Single Cell Whole Genome Amplification. PLoS ONE, 2011, 6, e26161.	1.1	163
15	A phylogenomic and ecological analysis of the globally abundant Marine Group II archaea (<i>Candidatus</i> Thaumarchaeum ETQq1). Nature Microbiology, 2021, 6, 958-968.	4.4	158
16	The importance of designating type material for uncultured taxa. Systematic and Applied Microbiology, 2019, 42, 15-21.	1.2	149
17	Impact of single-cell genomics and metagenomics on the emerging view of extremophile "microbial dark matter". Extremophiles, 2014, 18, 865-875.	0.9	133
18	Stop codon reassignments in the wild. Science, 2014, 344, 909-913.	6.0	124

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19	Single-cell genomics reveals complex carbohydrate degradation patterns in poribacterial symbionts of marine sponges. <i>ISME Journal</i> , 2013, 7, 2287-2300.	4.4	113
20	In Silico Analysis of the Metabolic Potential and Niche Specialization of Candidate Phylum "Latescibacteria" (WS3). <i>PLoS ONE</i> , 2015, 10, e0127499.	1.1	102
21	Undinarchaeota illuminate DPANN phylogeny and the impact of gene transfer on archaeal evolution. <i>Nature Communications</i> , 2020, 11, 3939.	5.8	102
22	Diverse Marinimicrobia bacteria may mediate coupled biogeochemical cycles along eco-thermodynamic gradients. <i>Nature Communications</i> , 2017, 8, 1507.	5.8	99
23	Defining the human gut host-phage network through single-cell viral tagging. <i>Nature Microbiology</i> , 2019, 4, 2192-2203.	5.9	95
24	Insights into the metabolism, lifestyle and putative evolutionary history of the novel archaeal phylum "Diapherotrites"™. <i>ISME Journal</i> , 2015, 9, 447-460.	4.4	89
25	"Candidatus Thiobios zoothamnicoli," an Ectosymbiotic Bacterium Covering the Giant Marine Ciliate <i>Zoothamnium niveum</i> . <i>Applied and Environmental Microbiology</i> , 2006, 72, 2014-2021.	1.4	84
26	The Candidate Phylum Poribacteria by Single-Cell Genomics: New Insights into Phylogeny, Cell-Compartmentation, Eukaryote-Like Repeat Proteins, and Other Genomic Features. <i>PLoS ONE</i> , 2014, 9, e87353.	1.1	79
27	Genomic Analysis of <i>Caldithrix abyssi</i> , the Thermophilic Anaerobic Bacterium of the Novel Bacterial Phylum Calditrarchaeota. <i>Frontiers in Microbiology</i> , 2017, 8, 195.	1.5	66
28	ProDeGe: a computational protocol for fully automated decontamination of genomes. <i>ISME Journal</i> , 2016, 10, 269-272.	4.4	65
29	Validation of picogram- and femtogram-input DNA libraries for microscale metagenomics. <i>PeerJ</i> , 2016, 4, e2486.	0.9	64
30	A microfluidics-based in situ chemotaxis assay to study the behaviour of aquatic microbial communities. <i>Nature Microbiology</i> , 2017, 2, 1344-1349.	5.9	60
31	Reconstructing each cell's genome within complex microbial communities—dream or reality?. <i>Frontiers in Microbiology</i> , 2014, 5, 771.	1.5	58
32	Chemotaxis shapes the microscale organization of the ocean's microbiome. <i>Nature</i> , 2022, 605, 132-138.	13.7	51
33	Molecular characterization of the symbionts associated with marine nematodes of the genus <i>Robbea</i> . <i>Environmental Microbiology Reports</i> , 2009, 1, 136-144.	1.0	46
34	High genetic similarity between two geographically distinct strains of the sulfur-oxidizing symbiont "Candidatus Thiobios zoothamnicoli"™. <i>FEMS Microbiology Ecology</i> , 2009, 67, 229-241.	1.3	35
35	Recoding of stop codons expands the metabolic potential of two novel Asgardarchaeota lineages. <i>ISME Communications</i> , 2021, 1, .	1.7	23
36	The effects of sulphide on growth and behaviour of the thiotrophic <i>Zoothamnium niveum</i> symbiosis. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2007, 274, 2259-2269.	1.2	22

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37	acdc " Automated Contamination Detection and Confidence estimation for single-cell genome data. BMC Bioinformatics, 2016, 17, 543.	1.2	22
38	Three families of Asgard archaeal viruses identified in metagenome-assembled genomes. Nature Microbiology, 2022, 7, 962-973.	5.9	21
39	Pathways, activities and thermal stability of anaerobic and aerobic enzymes in thermophilic vent paralvinellid worms. Marine Ecology - Progress Series, 2009, 382, 99-112.	0.9	11
40	Insights into plastic biodegradation: community composition and functional capabilities of the superworm (Zophobas morio) microbiome in styrofoam feeding trials. Microbial Genomics, 2022, 8, .	1.0	11
41	Microvolume DNA extraction methods for microscale amplicon and metagenomic studies. ISME Communications, 2021, 1, .	1.7	10
42	Macro camera temperature logger array for deep-sea hydrothermal vent and benthic studies. Limnology and Oceanography: Methods, 2009, 7, 527-534.	1.0	6
43	Single-Cell Genomics of Microbial Dark Matter. Methods in Molecular Biology, 2018, 1849, 99-111.	0.4	5
44	Cell proliferation and growth in Zoothamnium niveum (Oligohymenophora, Peritrichida) " Thiotrophic bacteria symbiosis. Symbiosis, 2009, 47, 43-50.	1.2	4
45	Editorial: Ecology, Metabolism and Evolution of Archaea-Perspectives From Proceedings of the International Workshop on Geo-Omics of Archaea. Frontiers in Microbiology, 2021, 12, 827229.	1.5	3